

Page 40, line 3, after "an", delete "A.", insert--A.--

Page 40, line 4, delete "tumefaciens", insert--*tumefaciens*--.

Page 40, line 6, after "of", delete "cocultivation", insert--co-cultivation--.

Page 40, line 9, after "28±2°C,", delete "30μE", insert--30 μE m<sup>-2</sup>s<sup>-1</sup>--.

Page 40, line 14, after "NH<sub>4</sub>Cl:", delete "B5", insert--B<sub>5</sub>--.

Page 40, line 15, after "mg/L", delete "carb", insert--carbenicillin--.

Page 40, line 27, after "80-85°", insert--F--.

#### In the claims

153  
C1  
1. (Amended) A DNA sequence comprising as operably joined components in the direction of transcription, a cotton fiber transcriptional factor functional in a cotton fiber cell and an open reading frame encoding a protein [of interest,] in a pigment biosynthesis pathway wherein said transcriptional factor is selected from the 4-4 and the *rac* promoter sequences and is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO:1 or SEQ ID NO:7 or SEQ ID NO: 12 or SEQ ID NO: 15 or SEQ ID NO: 16 and isolating a nucleotide sequence which has promoter activity from the 5' flanking region of genomic DNA which specifically hybridizes to said probe, whereby said transcriptional factor is obtained.

2. (Reiterated) The DNA sequence according to Claim 1, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.

Sub F3  
3. (Amended) The DNA sequence according to Claim 2, wherein said transport signal encoding sequence comprises a plastid transit [peptid] peptide.

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4. (Amended) The DNA sequence according to Claim 1, wherein said DNA sequence further comprises as an operably joined component a transport signal encoding sequence [encodes] for a signal peptide which provides for transport across the rough endoplasmic reticulum.

7. (Amended) The DNA sequence of Claim 1 wherein said open reading frame is from a bacterial or a plant gene.

8. (Amended) The DNA sequence of Claim 7 wherein said [bacterial] gene is selected from the group consisting of ORF438, *tyrA*, anthocyanin R gene, anthocyanin C1 gene, *pig*, and *tna*.

Sub 12 28  
134 9. (Amended) A DNA construct comprising a [promoter for transcription in a plant cell operably joined to said] DNA sequence of Claim 1.

Sub #57 10. (Amended) A DNA construct [of Claim 9 wherein said plant cell is a cotton fiber cell] comprising two DNA sequences according to Claim 1, wherein said protein in a biosynthesis pathway in each of said two DNA sequences is not encoded by the same gene.

Cancel claim 11. [11. The DNA construct of Claim 10 wherein said promoter is a tomato 4-4 and rac promoter.]

12. (Reiterated) A plant cell comprising a DNA construct of Claim 9.

13. (Reiterated) A plant comprising a plant cell of Claim 12.

Sub 14. (Amended) A method of modifying fiber phenotype in a cotton plant, said method comprising:  
D10

134 transforming a plant cell with a DNA [comprising a] construct [for] according to Claim 9 or 10 [for expression of a protein in a pigment biosynthesis pathway, wherein said construct comprises as operably joined components:

a transcriptional initiation region functional in cells of said plant tissue,  
an open reading frame encoding a protein of interest, and

Sub  
D10

a transcriptional initiation region functional in cells of said plant tissue,  
an open reading frame encoding a protein of interest, and  
a transcriptional termination region functional in cells of said plant tissue, wherein said  
plant tissue comprises a substrate of said protein] according to Claim 9 or 10; and  
growing said plant cell to produce a plant comprising said fiber tissue, wherein said plant  
tissue comprises a substrate of said protein of interest, and wherein said protein reacts with said  
substrate to produce said pigment, whereby the phenotype of said fiber is modified.

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15. (Amended) The method of Claim 14 [further comprising] wherein said DNA construct  
further comprises a transport signal encoding sequence from a plant nuclear-encoded gene.

16. (Amended) The method of Claim 14 wherein said DNA construct further comprises a  
transport signal encoding sequence, which encodes a signal peptide which provides for transport  
across the rough endoplasmic reticulum.

Cancel Claim 17.

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18. (Amended) ~~The method of Claim 16 wherein said DNA comprises constructs for~~  
~~expression of two proteins in a pigment biosynthesis pathway [, wherein each of said constructs~~  
~~comprises said components i) through iv), and] wherein said two proteins are not encoded by the~~  
~~same gene.~~

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19. (Amended) The method of Claim [17 or] 18 wherein said pigment is melanin and said  
proteins are encoded by *tyrA* and ORF438.

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20. (Amended) The method of Claim [17] 18 wherein said pigment is indigo and said  
proteins are encoded by *tna* and *pig*.

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21. (Amended) The method of Claim [17] <sup>43</sup>18 wherein said pigment is [anthocyanin] anthocyanin and said [constructs comprise] two proteins are the anthocyanin R and C1 [regulatory genes] proteins.

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Fig 7 22. (Amended) The method of Claim 14 wherein said [plant] fiber tissue is a cotton burr.

23. (Amended) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in [Figure 2] SEQ ID NO: 7.

24. (Amended) A recombinant DNA construct comprising the cotton tissue transcriptional sequence shown in [Figure 5] SEQ ID NO: 15.

157 25. (Amended) An isolated DNA [encoding] comprising the nucleotide sequence [of Figure] shown in SEQ ID NO: 1.

26. (Amended) An isolated DNA [encoding] comprising the nucleotide sequence [of Figure 4] shown in SEQ ID NO: 12.

27. (Amended) The method of Claim 14 wherein said protein [of interest] is [involved in the synthesis of] an enzyme in the biosynthetic or degradation pathway of a plant [hormone] pigment.

Add the following new claims.

Sub  
D' 28. The DNA sequence according to Claim 1 wherein said plant fiber tissue is cotton fiber tissue.

138 29. The DNA sequence according to Claim 28 wherein said transcription factor is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 12, and SEQ ID NO: 16.

transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ.ID NO:2 or. SEQ.ID NO:5 or SEQ.ID NO:XXX(Fig. 7)XXX. Add claim.s

31. <sup>30</sup> The DNA Sequence according to Claim 30, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.

32. <sup>30</sup> The DNA sequence according to Claim 31, wherein said transport signal encoding sequence comprises a plastid transit peptide.

33. <sup>32</sup> The DNA sequence according to Claim 30, further comprising a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.

34. <sup>32</sup> The DNA sequence according to Claim 33, wherein said sequence further comprises, 3' to said open reading frame, a vacuolar localization signal.

35. <sup>34</sup> The DNA sequence of Claim 34 wherein said open reading frame is from a bacterial gene.

36. <sup>34</sup> The DNA sequence of Claim 35 wherein said gene is selected from the group consisting of ORE438, *tyrA*, *pig*, and *tna*.

37. <sup>34</sup> A DNA construct comprising a DNA sequence of Claim 30.

38. <sup>36</sup> The DNA construct of Claim 37 wherein said plant cell is a cotton fiber cell.

39. <sup>38</sup> A plant cell comprising a DNA construct of Claim 37.

40. <sup>39</sup> A plant comprising a plant cell of Claim 39.

B

<sup>439</sup>  
39. A plant cell comprising a DNA construct of Claim <sup>37</sup>37.

<sup>44</sup>  
40. A plant comprising a plant cell of Claim <sup>39</sup>39.

<sup>442</sup>  
41. The DNA sequence according to Claim 30 wherein said plant fiber tissue is cotton fiber tissue.

<sup>443</sup>  
42. The DNA sequence according to Claim <sup>41</sup>41 wherein said transcription factor is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, SEQ ID NO: 11, SEQ ID NO: 12, and SEQ ID NO: 16.

<sup>444</sup>  
43. A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional factor functional in a cotton fiber cell and an open reading frame encoding an enzyme in a biosynthetic or degradation pathway of melanin or indigo, wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO: 1 or SEQ ID NO: 7 or SEQ ID NO: 11 or SEQ ID NO: 12 or SEQ ID NO: 16.

<sup>445</sup>  
44. The DNA sequence according to Claim <sup>43</sup>43, further comprising a transport signal encoding sequence from a plant nuclear-encoded gene.

<sup>446</sup>  
45. The DNA sequence according to Claim <sup>44</sup>44, wherein said transport signal encoding sequence comprises a plastid transit peptide.

<sup>447</sup>  
46. The DNA sequence according to Claim <sup>45</sup>45, further comprising a transport signal encoding sequence for a signal peptide which provides for transport across the rough endoplasmic reticulum.

<sup>448</sup>  
47. The DNA sequence according to Claim <sup>46</sup>46, wherein said sequence further comprises, 3' to said open reading frame, a vacuolar localization signal.

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48. The DNA sequence of Claim 43 wherein said open reading frame is from a bacterial

gene.

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The DNA sequence of Claim 48 wherein said gene is selected from the group consisting of ORF438, *tyrA*, *pig*, and *tna*.

Sub F21 50. A DNA construct comprising a DNA sequence of Claim 43.

Sub D17 51. The DNA construct of Claim 50 wherein said plant cell is a cotton fiber cell.

Sub B8 F22 52. A plant cell comprising a DNA construct of Claim 50.

53. A plant comprising a plant cell of Claim 52.

Sub D18 54. The DNA sequence according to Claim 43 wherein said plant fiber tissue is cotton fiber tissue.

55. The DNA sequence according to Claim 54 wherein said transcription factor is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 7, or SEQ ID NO: 16.

Sub D19 56. A DNA sequence comprising as operably joined components in the direction of transcription, a transcriptional factor functional in a cotton fiber cell and an open reading frame encoding an enzyme in the biosynthetic pathway of a pigment, wherein said transcriptional factor is obtained by the method of probing a genomic library derived from a plant fiber tissue with up to the full length of a probe derived from the cDNA sequence shown in SEQ ID NO: 1 or SEQ ID NO: 7 or SEQ ID NO: 16--.